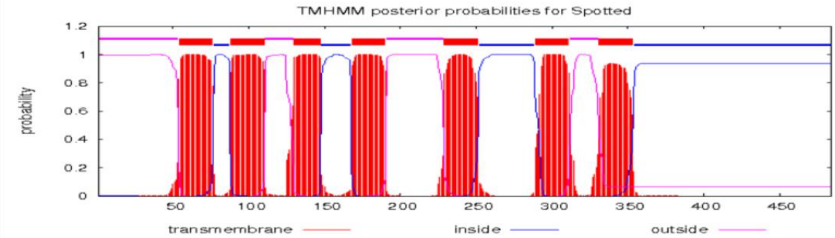
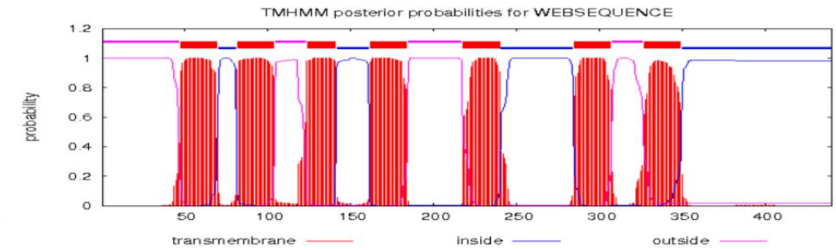
A

```
# Spotted Length: 484
# Spotted Number of predicted TMHs:  7
# Spotted Exp number of AAs in TMHs: 154.5427
# Spotted Exp number, first 60 AAs:  7.49391
# Spotted Total prob of N-in:        0.00287
Spotted TMHMM2.0          outside      1    53
Spotted TMHMM2.0          TMhelix     54    76
Spotted TMHMM2.0          inside      77    87
Spotted TMHMM2.0          TMhelix     88   110
Spotted TMHMM2.0          outside    111   129
Spotted TMHMM2.0          TMhelix    130   147
Spotted TMHMM2.0          inside     148   167
Spotted TMHMM2.0          TMhelix    168   190
Spotted TMHMM2.0          outside    191   228
Spotted TMHMM2.0          TMhelix    229   251
Spotted TMHMM2.0          inside     252   288
Spotted TMHMM2.0          TMhelix    289   311
Spotted TMHMM2.0          outside    312   330
Spotted TMHMM2.0          TMhelix    331   353
Spotted TMHMM2.0          inside     354   484
```



B

```
# WEBSEQUENCE Length: 440
# WEBSEQUENCE Number of predicted TMHs:  7
# WEBSEQUENCE Exp number of AAs in TMHs: 155.73197
# WEBSEQUENCE Exp number, first 60 AAs:  13.97193
# WEBSEQUENCE Total prob of N-in:        0.00009
# WEBSEQUENCE POSSIBLE N-term signal sequence
WEBSEQUENCE      TMHMM2.0          outside      1    47
WEBSEQUENCE      TMHMM2.0          TMhelix     48    70
WEBSEQUENCE      TMHMM2.0          inside      71    81
WEBSEQUENCE      TMHMM2.0          TMhelix     82   104
WEBSEQUENCE      TMHMM2.0          outside    105   123
WEBSEQUENCE      TMHMM2.0          TMhelix    124   141
WEBSEQUENCE      TMHMM2.0          inside     142   161
WEBSEQUENCE      TMHMM2.0          TMhelix    162   184
WEBSEQUENCE      TMHMM2.0          outside    185   217
WEBSEQUENCE      TMHMM2.0          TMhelix    218   240
WEBSEQUENCE      TMHMM2.0          inside     241   284
WEBSEQUENCE      TMHMM2.0          TMhelix    285   307
WEBSEQUENCE      TMHMM2.0          outside    308   326
WEBSEQUENCE      TMHMM2.0          TMhelix    327   349
WEBSEQUENCE      TMHMM2.0          inside     350   440
```



C

```
# WEBSEQUENCE Length: 440
# WEBSEQUENCE Number of predicted TMHs:  7
# WEBSEQUENCE Exp number of AAs in TMHs: 155.73197
# WEBSEQUENCE Exp number, first 60 AAs:  13.97193
# WEBSEQUENCE Total prob of N-in:        0.00009
# WEBSEQUENCE POSSIBLE N-term signal sequence
WEBSEQUENCE      TMHMM2.0          outside      1    47
WEBSEQUENCE      TMHMM2.0          TMhelix     48    70
WEBSEQUENCE      TMHMM2.0          inside      71    81
WEBSEQUENCE      TMHMM2.0          TMhelix     82   104
WEBSEQUENCE      TMHMM2.0          outside    105   123
WEBSEQUENCE      TMHMM2.0          TMhelix    124   141
WEBSEQUENCE      TMHMM2.0          inside     142   161
WEBSEQUENCE      TMHMM2.0          TMhelix    162   184
WEBSEQUENCE      TMHMM2.0          outside    185   217
WEBSEQUENCE      TMHMM2.0          TMhelix    218   240
WEBSEQUENCE      TMHMM2.0          inside     241   284
WEBSEQUENCE      TMHMM2.0          TMhelix    285   307
WEBSEQUENCE      TMHMM2.0          outside    308   326
WEBSEQUENCE      TMHMM2.0          TMhelix    327   349
WEBSEQUENCE      TMHMM2.0          inside     350   440
```

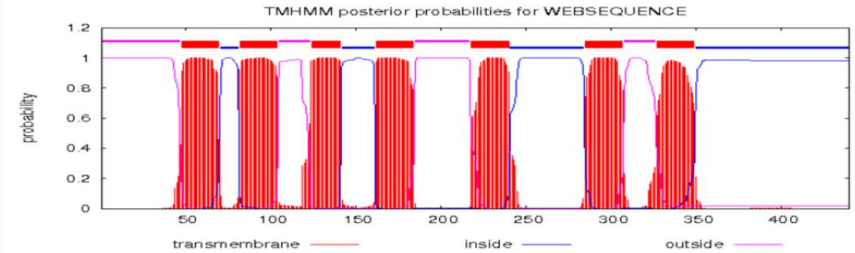


Fig.S1. Seven transmembrane region of NPFFR1, NPFFR2-1 and NPFFR2-2. (**A**) NPFFR1. Transmembrane region of the spotted sea bass amino acids sequence. (**B**) and (**C**) NPFFR2-1 and NPFFR2-2.